SEQUENCE LISTING

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Daigo, Yataro
Nakatsuru, Shuichi

<120> METHOD FOR DIAGNOSING NON-SMALL CELL LUNG CANCER

<130> 082368-000510US

<150> PCT/JP2005/005613
<151> 2005-03-18

<150> US 60/555,789
<151> 2004-03-23

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<170> PatentIn version 3.3

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Lys Glu Glu Lys Gly Lys Asn Ile Gln Val Val Val Arg Cys Arg Pro
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Phe Asn Leu Ala Glu Arg Lys Ala Ser Ala His Ser Ile Val Glu Cys
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Asp Pro Val Arg Lys Glu Val Ser Val Arg Thr Gly Gly Leu Ala Asp
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aag agc tca agg aaa aca tac act ttt gat atg gtg ttt gga gca tct 365
Lys Ser Ser Arg Lys Thr Tyr Thr Phe Asp Met Val Phe Gly Ala Ser
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act aaa cag att gat gtt tac cga agt gtt gtt tgt cca att ctg gat 413
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Gly Thr Gly Lys Thr Phe Thr Met Glu Gly Glu Arg Ser Pro Asn Glu
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gag tat acc tgg gaa gag gat ccc ttg gct ggt ata att cca cgt acc      557
Glu Tyr Thr Trp Glu Glu Asp Pro Leu Ala Gly Ile Ile Pro Arg Thr
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ctt cat caa att ttt gag aaa ctt act gat aat ggt act gaa ttt tca      605
Leu His Gln Ile Phe Glu Lys Leu Thr Asp Asn Gly Thr Glu Phe Ser
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gtc aaa gtg tct ctg ttg gag atc tat aat gaa gag ctt ttt gat ctt      653
Val Lys Val Ser Leu Leu Glu Ile Tyr Asn Glu Glu Leu Phe Asp Leu
                160                 165                 170

ctt aat cca tca tct gat gtt tct gag aga cta cag atg ttt gat gat      701
Leu Asn Pro Ser Ser Asp Val Ser Glu Arg Leu Gln Met Phe Asp Asp
          175                 180                 185

ccc cgt aac aag aga gga gtg ata att aaa ggt tta gaa gaa att aca      749
Pro Arg Asn Lys Arg Gly Val Ile Ile Lys Gly Leu Glu Glu Ile Thr
        190                 195                 200

gta cac aac aag gat gaa gtc tat caa att tta gaa aag ggg gca gca      797
Val His Asn Lys Asp Glu Val Tyr Gln Ile Leu Glu Lys Gly Ala Ala
    205                 210                 215

aaa agg aca act gca gct act ctg atg aat gca tac tct agt cgt tcc      845
Lys Arg Thr Thr Ala Ala Thr Leu Met Asn Ala Tyr Ser Ser Arg Ser
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cac tca gtt ttc tct gtt aca ata cat atg aaa gaa act acg att gat      893
His Ser Val Phe Ser Val Thr Ile His Met Lys Glu Thr Thr Ile Asp
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gga gaa gag ctt gtt aaa atc gga aag ttg aac ttg gtt gat ctt gca      941
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          255                 260                 265

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Glu Ala Gly Asn Ile Asn Gln Ser Leu Leu Thr Leu Gly Arg Val Ile
    285                 290                 295

act gcc ctt gta gaa aga aca cct cat gtt cct tat cga gaa tct aaa     1085
Thr Ala Leu Val Glu Arg Thr Pro His Val Pro Tyr Arg Glu Ser Lys
300                 305                 310                 315

cta act aga atc ctc cag gat tct ctt gga ggg cgt aca aga aca tct     1133
Leu Thr Arg Ile Leu Gln Asp Ser Leu Gly Gly Arg Thr Arg Thr Ser
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agt aca ttg gaa tat gct cat aga gca aag aac ata ttg aat aag cct     1229
Ser Thr Leu Glu Tyr Ala His Arg Ala Lys Asn Ile Leu Asn Lys Pro
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gaa gtg aat cag aaa ctc acc aaa aaa gct ctt att aag gag tat acg     1277
Glu Val Asn Gln Lys Leu Thr Lys Lys Ala Leu Ile Lys Glu Tyr Thr
    365                 370                 375

gag gag ata gaa cgt tta aaa cga gat ctt gct gca gcc cgt gag aaa     1325
Glu Glu Ile Glu Arg Leu Lys Arg Asp Leu Ala Ala Ala Arg Glu Lys
380                 385                 390                 395

aat gga gtg tat att tct gaa gaa aat ttt aga gtc atg agt gga aaa     1373
Asn Gly Val Tyr Ile Ser Glu Glu Asn Phe Arg Val Met Ser Gly Lys
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tta act gtt caa gaa gag cag att gta gaa ttg att gaa aaa att ggt     1421
Leu Thr Val Gln Glu Glu Gln Ile Val Glu Leu Ile Glu Lys Ile Gly
            415                 420                 425

gct gtt gag gag gag ctg aat agg gtt aca gag ttg ttt atg gat aat     1469
Ala Val Glu Glu Glu Leu Asn Arg Val Thr Glu Leu Phe Met Asp Asn
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aaa aat gaa ctt gac cag tgt aaa tct gac ctg caa aat aaa aca caa     1517
Lys Asn Glu Leu Asp Gln Cys Lys Ser Asp Leu Gln Asn Lys Thr Gln
    445                 450                 455

gaa ctt gaa acc act caa aaa cat ttg caa gaa act aaa tta caa ctt     1565
Glu Leu Glu Thr Thr Gln Lys His Leu Gln Glu Thr Lys Leu Gln Leu
460                 465                 470                 475

gtt aaa gaa gaa tat atc aca tca gct ttg gaa agt act gag gag aaa     1613
Val Lys Glu Glu Tyr Ile Thr Ser Ala Leu Glu Ser Thr Glu Glu Lys
                480                 485                 490

ctt cat gat gct gcc agc aag ctg ctt aac aca gtt gaa gaa act aca     1661
Leu His Asp Ala Ala Ser Lys Leu Leu Asn Thr Val Glu Glu Thr Thr
            495                 500                 505

aaa gat gta tct ggt ctc cat tcc aaa ctg gat cgt aag aag gca gtt     1709
Lys Asp Val Ser Gly Leu His Ser Lys Leu Asp Arg Lys Lys Ala Val
        510                 515                 520

gac caa cac aat gca gaa gct cag gat att ttt ggc aaa aac ctg aat     1757
Asp Gln His Asn Ala Glu Ala Gln Asp Ile Phe Gly Lys Asn Leu Asn
    525                 530                 535

agt ctg ttt aat aat atg gaa gaa tta att aag gat ggc agc tca aag     1805
Ser Leu Phe Asn Asn Met Glu Glu Leu Ile Lys Asp Gly Ser Ser Lys
540                 545                 550                 555

caa aag gcc atg cta gaa gta cat aag acc tta ttt ggt aat ctg ctg     1853
Gln Lys Ala Met Leu Glu Val His Lys Thr Leu Phe Gly Asn Leu Leu
                560                 565                 570

tct tcc agt gtc tct gca tta gat acc att act aca gta gca ctt gga     1901
Ser Ser Ser Val Ser Ala Leu Asp Thr Ile Thr Thr Val Ala Leu Gly
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tct ctc aca tct att cca gaa aat gtg tct act cat gtt tct cag att     1949
Ser Leu Thr Ser Ile Pro Glu Asn Val Ser Thr His Val Ser Gln Ile
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ttt aat atg ata cta aaa gaa caa tca tta gca gca gaa agt aaa act     1997
Phe Asn Met Ile Leu Lys Glu Gln Ser Leu Ala Ala Glu Ser Lys Thr
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gta cta cag gaa ttg att aat gta ctc aag act gat ctt cta agt tca     2045
Val Leu Gln Glu Leu Ile Asn Val Leu Lys Thr Asp Leu Leu Ser Ser
620                 625                 630                 635

ctg gaa atg att tta tcc cca act gtg gtg tct ata ctg aaa atc aat     2093
Leu Glu Met Ile Leu Ser Pro Thr Val Val Ser Ile Leu Lys Ile Asn
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agt caa cta aag cat att ttc aag act tca ttg aca gtg gcc gat aag     2141
Ser Gln Leu Lys His Ile Phe Lys Thr Ser Leu Thr Val Ala Asp Lys
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ata gaa gat caa aaa aag gaa cta gat ggc ttt ctc agt ata ctg tgt     2189
Ile Glu Asp Gln Lys Lys Glu Leu Asp Gly Phe Leu Ser Ile Leu Cys
        670                 675                 680

aac aat cta cat gaa cta caa gaa aat acc att tgt tcc ttg gtt gag     2237
Asn Asn Leu His Glu Leu Gln Glu Asn Thr Ile Cys Ser Leu Val Glu
    685                 690                 695

tca caa aag caa tgt gga aac cta act gaa gac ctg aag aca ata aag     2285
Ser Gln Lys Gln Cys Gly Asn Leu Thr Glu Asp Leu Lys Thr Ile Lys
700                 705                 710                 715

cag acc cat tcc cag gaa ctt tgc aag tta atg aat ctt tgg aca gag     2333
Gln Thr His Ser Gln Glu Leu Cys Lys Leu Met Asn Leu Trp Thr Glu
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aga ttc tgt gct ttg gag gaa aag tgt gaa aat ata cag aaa cca ctt     2381
Arg Phe Cys Ala Leu Glu Glu Lys Cys Glu Asn Ile Gln Lys Pro Leu
            735                 740                 745

agt agt gtc cag gaa aat ata cag cag aaa tct aag gat ata gtc aac     2429
Ser Ser Val Gln Glu Asn Ile Gln Gln Lys Ser Lys Asp Ile Val Asn
        750                 755                 760

aaa atg act ttt cac agt caa aaa ttt tgt gct gat tct gat ggc ttc     2477
Lys Met Thr Phe His Ser Gln Lys Phe Cys Ala Asp Ser Asp Gly Phe
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tca cag gaa ctc aga aat ttt aac caa gaa ggt aca aaa ttg gtt gaa     2525
Ser Gln Glu Leu Arg Asn Phe Asn Gln Glu Gly Thr Lys Leu Val Glu
780                 785                 790                 795

gaa tct gtg aaa cac tct gat aaa ctc aat ggc aac ctg gaa aaa ata     2573
Glu Ser Val Lys His Ser Asp Lys Leu Asn Gly Asn Leu Glu Lys Ile
                800                 805                 810

tct caa gag act gaa cag aga tgt gaa tct ctg aac aca aga aca gtt     2621
Ser Gln Glu Thr Glu Gln Arg Cys Glu Ser Leu Asn Thr Arg Thr Val
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tat ttt tct gaa cag tgg gta tct tcc tta aat gaa agg gaa cag gaa     2669
Tyr Phe Ser Glu Gln Trp Val Ser Ser Leu Asn Glu Arg Glu Gln Glu
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ctt cac aac tta ttg gag gtt gta agc caa tgt tgt gag gct tca agt     2717
Leu His Asn Leu Leu Glu Val Val Ser Gln Cys Cys Glu Ala Ser Ser
    845                 850                 855

tca gac atc act gag aaa tca gat gga cgt aag gca gct cat gag aaa     2765
Ser Asp Ile Thr Glu Lys Ser Asp Gly Arg Lys Ala Ala His Glu Lys
860                 865                 870                 875

cag cat aac att ttt ctt gat cag atg act att gat gaa gat aaa ttg     2813
Gln His Asn Ile Phe Leu Asp Gln Met Thr Ile Asp Glu Asp Lys Leu
                880                 885                 890

ata gca caa aat cta gaa ctt aat gaa acc ata aaa att ggt ttg act     2861
Ile Ala Gln Asn Leu Glu Leu Asn Glu Thr Ile Lys Ile Gly Leu Thr
            895                 900                 905

aag ctt aat tgc ttt ctg gaa cag gat ctg aaa ctg gat atc cca aca     2909
Lys Leu Asn Cys Phe Leu Glu Gln Asp Leu Lys Leu Asp Ile Pro Thr
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ggt acg aca cca cag agg aaa agt tat tta tac cca tca aca ctg gta     2957
Gly Thr Thr Pro Gln Arg Lys Ser Tyr Leu Tyr Pro Ser Thr Leu Val
    925                 930                 935

aga act gaa cca cgt gaa cat ctc ctt gat cag ctg aaa agg aaa cag     3005
Arg Thr Glu Pro Arg Glu His Leu Leu Asp Gln Leu Lys Arg Lys Gln
940                 945                 950                 955

cct gag ctg tta atg atg cta aac tgt tca gaa aac aac aaa gaa gag     3053
Pro Glu Leu Leu Met Met Leu Asn Cys Ser Glu Asn Asn Lys Glu Glu
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aca att ccg gat gtg gat gta gaa gag gca gtt ctg ggg cag tat act     3101
Thr Ile Pro Asp Val Asp Val Glu Glu Ala Val Leu Gly Gln Tyr Thr
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tca tca  att ggc ggg gtt cca  ttt ttc cag cat aaa  aaa tca cat      3194
Ser Ser  Ile Gly Gly Val Pro  Phe Phe Gln His Lys  Lys Ser His
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gga aaa  gac aaa gaa aac aga  ggc att aac aca ctg  gag agg tct      3239
Gly Lys  Asp Lys Glu Asn Arg  Gly Ile Asn Thr Leu  Glu Arg Ser
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aaa gtg  gaa gaa act aca gag  cac ttg gtt aca aag  agc aga tta      3284
Lys Val  Glu Glu Thr Thr Glu  His Leu Val Thr Lys  Ser Arg Leu
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Glu Val Ser Val Arg Thr Gly Gly Leu Ala Asp Lys Ser Ser Arg Lys
50 55 60

Thr Tyr Thr Phe Asp Met Val Phe Gly Ala Ser Thr Lys Gln Ile Asp
65 70 75 80

Val Tyr Arg Ser Val Val Cys Pro Ile Leu Asp Glu Val Ile Met Gly
85 90 95

Tyr Asn Cys Thr Ile Phe Ala Tyr Gly Gln Thr Gly Thr Gly Lys Thr
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Phe Thr Met Glu Gly Glu Arg Ser Pro Asn Glu Glu Tyr Thr Trp Glu
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Glu Asp Pro Leu Ala Gly Ile Ile Pro Arg Thr Leu His Gln Ile Phe
130 135 140

Glu Lys Leu Thr Asp Asn Gly Thr Glu Phe Ser Val Lys Val Ser Leu
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Leu Glu Ile Tyr Asn Glu Glu Leu Phe Asp Leu Leu Asn Pro Ser Ser
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Asp Val Ser Glu Arg Leu Gln Met Phe Asp Asp Pro Arg Asn Lys Arg
180 185 190

Gly Val Ile Ile Lys Gly Leu Glu Glu Ile Thr Val His Asn Lys Asp
195 200 205

Glu Val Tyr Gln Ile Leu Glu Lys Gly Ala Ala Lys Arg Thr Thr Ala
210 215 220

Ala Thr Leu Met Asn Ala Tyr Ser Ser Arg Ser His Ser Val Phe Ser
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Val Thr Ile His Met Lys Glu Thr Thr Ile Asp Gly Glu Glu Leu Val

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Lys Ile Gly Lys Leu Asn Leu Val Asp Leu Ala Gly Ser Glu Asn Ile
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Gly Arg Ser Gly Ala Val Asp Lys Arg Ala Arg Glu Ala Gly Asn Ile
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Arg Thr Pro His Val Pro Tyr Arg Glu Ser Lys Leu Thr Arg Ile Leu
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Gln Asp Ser Leu Gly Gly Arg Thr Arg Thr Ser Ile Ile Ala Thr Ile
325 330 335

Ser Pro Ala Ser Leu Asn Leu Glu Glu Thr Leu Ser Thr Leu Glu Tyr
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Ala His Arg Ala Lys Asn Ile Leu Asn Lys Pro Glu Val Asn Gln Lys
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Leu Thr Lys Lys Ala Leu Ile Lys Glu Tyr Thr Glu Glu Ile Glu Arg
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Glu Gln Ile Val Glu Leu Ile Glu Lys Ile Gly Ala Val Glu Glu Glu
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Leu His Ser Lys Leu Asp Arg Lys Lys Ala Val Asp Gln His Asn Ala
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Glu Val His Lys Thr Leu Phe Gly Asn Leu Leu Ser Ser Ser Val Ser
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Ser Gln Lys Phe Cys Ala Asp Ser Asp Gly Phe Ser Gln Glu Leu Arg
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785 790 795 800

Ser Asp Lys Leu Asn Gly Asn Leu Glu Lys Ile Ser Gln Glu Thr Glu
805 810 815

Gln Arg Cys Glu Ser Leu Asn Thr Arg Thr Val Tyr Phe Ser Glu Gln
820 825 830

Trp Val Ser Ser Leu Asn Glu Arg Glu Gln Glu Leu His Asn Leu Leu
835 840 845

Glu Val Val Ser Gln Cys Cys Glu Ala Ser Ser Ser Asp Ile Thr Glu
850 855 860

Lys Ser Asp Gly Arg Lys Ala Ala His Glu Lys Gln His Asn Ile Phe
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Leu Asp Gln Met Thr Ile Asp Glu Asp Lys Leu Ile Ala Gln Asn Leu
885 890 895

Glu Leu Asn Glu Thr Ile Lys Ile Gly Leu Thr Lys Leu Asn Cys Phe
900 905 910

Leu Glu Gln Asp Leu Lys Leu Asp Ile Pro Thr Gly Thr Thr Pro Gln
915 920 925

Arg Lys Ser Tyr Leu Tyr Pro Ser Thr Leu Val Arg Thr Glu Pro Arg
930 935 940

Glu His Leu Leu Asp Gln Leu Lys Arg Lys Gln Pro Glu Leu Leu Met
945 950 955 960

Met Leu Asn Cys Ser Glu Asn Asn Lys Glu Glu Thr Ile Pro Asp Val
965 970 975

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Asp Val Glu Glu Ala Val Leu Gly Gln Tyr Thr Glu Glu Pro Leu Ser
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Gln Glu Pro Ser Val Asp Ala Gly  Val Asp Cys Ser Ser  Ile Gly Gly
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Val Pro  Phe Phe Gln His Lys  Lys Ser His Gly Lys  Asp Lys Glu
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Asn Arg  Gly Ile Asn Thr Leu  Glu Arg Ser Lys Val  Glu Glu Thr
    1025                1030                1035

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gcc gac ctg gac tgg gat gct tcc ccc ggc aac gac tcg ctg ggc gac       96
Ala Asp Leu Asp Trp Asp Ala Ser Pro Gly Asn Asp Ser Leu Gly Asp
            20                  25                  30

gag ctg ctg cag ctc ttc ccc gcg ccg ctg ctg gcg ggc gtc aca gcc      144
Glu Leu Leu Gln Leu Phe Pro Ala Pro Leu Leu Ala Gly Val Thr Ala
        35                  40                  45

acc tgc gtg gca ctc ttc gtg gtg ggt atc gct ggc aac ctg ctc acc      192
Thr Cys Val Ala Leu Phe Val Val Gly Ile Ala Gly Asn Leu Leu Thr
    50                  55                  60

atg ctg gtg gtg tcg cgc ttc cgc gag ctg cgc acc acc acc aac ctc      240
Met Leu Val Val Ser Arg Phe Arg Glu Leu Arg Thr Thr Thr Asn Leu
65                  70                  75                  80

tac ctg tcc agc atg gcc ttc tcc gat ctg ctc atc ttc ctc tgc atg      288
Tyr Leu Ser Ser Met Ala Phe Ser Asp Leu Leu Ile Phe Leu Cys Met
                85                  90                  95

ccc ctg gac ctc gtt cgc ctc tgg cag tac cgg ccc tgg aac ttc ggc      336
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gac ctc ctc tgc aaa ctc ttc caa ttc gtc agt gag agc tgc acc tac      384
Asp Leu Leu Cys Lys Leu Phe Gln Phe Val Ser Glu Ser Cys Thr Tyr
        115                 120                 125

gcc acg gtg ctc acc atc aca gcg ctg agc gtc gag cgc tac ttc gcc      432
Ala Thr Val Leu Thr Ile Thr Ala Leu Ser Val Glu Arg Tyr Phe Ala
    130                 135                 140

atc tgc ttc cca ctc cgg gcc aag gtg gtg gtc acc aag ggg cgg gtg      480
Ile Cys Phe Pro Leu Arg Ala Lys Val Val Val Thr Lys Gly Arg Val
145                 150                 155                 160

aag ctg gtc atc ttc gtc atc tgg gcc gtg gcc ttc tgc agc gcc ggg      528
Lys Leu Val Ile Phe Val Ile Trp Ala Val Ala Phe Cys Ser Ala Gly
                165                 170                 175

ccc atc ttc gtg cta gtc ggg gtg gag cac gag aac ggc acc gac cct      576
Pro Ile Phe Val Leu Val Gly Val Glu His Glu Asn Gly Thr Asp Pro
            180                 185                 190

tgg gac acc aac gag tgc cgc ccc acc gag ttt gcg gtg cgc tct gga      624
Trp Asp Thr Asn Glu Cys Arg Pro Thr Glu Phe Ala Val Arg Ser Gly
        195                 200                 205

ctg ctc acg gtc atg gtg tgg gtg tcc agc atc ttc ttc ttc ctt cct      672
Leu Leu Thr Val Met Val Trp Val Ser Ser Ile Phe Phe Phe Leu Pro
    210                 215                 220

gtc ttc tgt ctc acg gtc ctc tac agt ctc atc ggc agg aag ctg tgg      720
Val Phe Cys Leu Thr Val Leu Tyr Ser Leu Ile Gly Arg Lys Leu Trp
225                 230                 235                 240

cgg agg agg cgc ggc gat gct gtc gtg ggt gcc tcg ctc agg gac cag      768
Arg Arg Arg Arg Gly Asp Ala Val Val Gly Ala Ser Leu Arg Asp Gln
                245                 250                 255

aac cac aag caa acc gtg aaa atg ctg ggt ggg tct cag cgc gcg ctc      816
Asn His Lys Gln Thr Val Lys Met Leu Gly Gly Ser Gln Arg Ala Leu
            260                 265                 270

agg ctt tct ctc gcg ggt cct atc ctc tcc ctg tgc ctt ctc cct tct      864
Arg Leu Ser Leu Ala Gly Pro Ile Leu Ser Leu Cys Leu Leu Pro Ser
        275                 280                 285

ctc tga                                                              870
Leu
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<210> 4
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<213> Homo sapiens

<400> 4

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Met Trp Asn Ala Thr Pro Ser Glu Glu Pro Gly Phe Asn Leu Thr Leu
1               5                   10                  15
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Ala Asp Leu Asp Trp Asp Ala Ser Pro Gly Asn Asp Ser Leu Gly Asp
            20                  25                  30

Glu Leu Leu Gln Leu Phe Pro Ala Pro Leu Leu Ala Gly Val Thr Ala
        35                  40                  45

Thr Cys Val Ala Leu Phe Val Val Gly Ile Ala Gly Asn Leu Leu Thr
    50                  55                  60

Met Leu Val Val Ser Arg Phe Arg Glu Leu Arg Thr Thr Thr Asn Leu
65                  70                  75                  80

Tyr Leu Ser Ser Met Ala Phe Ser Asp Leu Leu Ile Phe Leu Cys Met
                85                  90                  95

Pro Leu Asp Leu Val Arg Leu Trp Gln Tyr Arg Pro Trp Asn Phe Gly
            100                 105                 110

Asp Leu Leu Cys Lys Leu Phe Gln Phe Val Ser Glu Ser Cys Thr Tyr
        115                 120                 125

Ala Thr Val Leu Thr Ile Thr Ala Leu Ser Val Glu Arg Tyr Phe Ala
    130                 135                 140

Ile Cys Phe Pro Leu Arg Ala Lys Val Val Val Thr Lys Gly Arg Val
145                 150                 155                 160

Lys Leu Val Ile Phe Val Ile Trp Ala Val Ala Phe Cys Ser Ala Gly
                165                 170                 175

Pro Ile Phe Val Leu Val Gly Val Glu His Glu Asn Gly Thr Asp Pro
            180                 185                 190

Trp Asp Thr Asn Glu Cys Arg Pro Thr Glu Phe Ala Val Arg Ser Gly
        195                 200                 205

Leu Leu Thr Val Met Val Trp Val Ser Ser Ile Phe Phe Phe Leu Pro
    210                 215                 220

Val Phe Cys Leu Thr Val Leu Tyr Ser Leu Ile Gly Arg Lys Leu Trp
225                 230                 235                 240

Arg Arg Arg Arg Gly Asp Ala Val Val Gly Ala Ser Leu Arg Asp Gln
                245                 250                 255
```

```
Asn His Lys Gln Thr Val Lys Met Leu Gly Gly Ser Gln Arg Ala Leu
            260                 265                 270

Arg Leu Ser Leu Ala Gly Pro Ile Leu Ser Leu Cys Leu Leu Pro Ser
        275                 280                 285

Leu
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<400> 5

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cccgaggaac cacgggttct ggagctagga gccggaagct gggagtccgg aggagagcgg    180

agcccggagc ccggagcccg gggcggcgcg tctgggtctg gcgcttcccg actggacggc    240

gcgcccgctg gtcttcgcca cgcgccctcc cctgggctcg cgttcatcgg tccccgcctg    300

agacgcgccc actcctgccc ggacttccag ccccggaggc gccggacaga gccgcggact    360

ccagcgccca cc atg cgc ctc aac agc tcc gcg ccg gga acc ccg ggc acg    411
              Met Arg Leu Asn Ser Ser Ala Pro Gly Thr Pro Gly Thr
              1               5                   10

ccg gcc gcc gac ccc ttc cag cgg gcg cag gcc gga ctg gag gag gcg    459
Pro Ala Ala Asp Pro Phe Gln Arg Ala Gln Ala Gly Leu Glu Glu Ala
    15                  20                  25

ctg ctg gcc ccg ggc ttc ggc aac gct tcg ggc aac gcg tcg gag cgc    507
Leu Leu Ala Pro Gly Phe Gly Asn Ala Ser Gly Asn Ala Ser Glu Arg
30                  35                  40                  45

gtc ctg gcg gca ccc agc agc gag ctg gac gtg aac acc gac atc tac    555
Val Leu Ala Ala Pro Ser Ser Glu Leu Asp Val Asn Thr Asp Ile Tyr
                50                  55                  60

tcc aaa gtg ctg gtg acc gcc gtg tac ctg gcg ctc ttc gtg gtg ggc    603
Ser Lys Val Leu Val Thr Ala Val Tyr Leu Ala Leu Phe Val Val Gly
            65                  70                  75

acg gtg ggc aac acg gtg acg gcg ttc acg ctg gcg cgg aag aag tcg    651
Thr Val Gly Asn Thr Val Thr Ala Phe Thr Leu Ala Arg Lys Lys Ser
        80                  85                  90

ctg cag agc ctg cag agc acg gtg cat tac cac ctg ggc agc ctg gcg    699
Leu Gln Ser Leu Gln Ser Thr Val His Tyr His Leu Gly Ser Leu Ala
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    95                  100                 105

ctg tcc gac ctg ctc acc ctg ctg ctg gcc atg ccc gtg gag ctg tac      747
Leu Ser Asp Leu Leu Thr Leu Leu Leu Ala Met Pro Val Glu Leu Tyr
110                 115                 120                 125

aac ttc atc tgg gtg cac cac ccc tgg gcc ttc ggc gac gcc ggc tgc      795
Asn Phe Ile Trp Val His His Pro Trp Ala Phe Gly Asp Ala Gly Cys
                130                 135                 140

cgc ggc tac tac ttc ctg cgc gac gcc tgc acc tac gcc acg gcc ctc      843
Arg Gly Tyr Tyr Phe Leu Arg Asp Ala Cys Thr Tyr Ala Thr Ala Leu
            145                 150                 155

aac gtg gcc agc ctg agt gtg gag cgc tac ctg gcc atc tgc cac ccc      891
Asn Val Ala Ser Leu Ser Val Glu Arg Tyr Leu Ala Ile Cys His Pro
        160                 165                 170

ttc aag gcc aag acc ctc atg tcc cga agc cgc acc aag aag ttc atc      939
Phe Lys Ala Lys Thr Leu Met Ser Arg Ser Arg Thr Lys Lys Phe Ile
    175                 180                 185

agc gcc atc tgg ctc gcc tcg gcc ctg ctg acg gtg cct atg ctg ttc      987
Ser Ala Ile Trp Leu Ala Ser Ala Leu Leu Thr Val Pro Met Leu Phe
190                 195                 200                 205

acc atg ggc gag cag aac cgc agc gcc gac ggc cag cac gcc ggc ggc     1035
Thr Met Gly Glu Gln Asn Arg Ser Ala Asp Gly Gln His Ala Gly Gly
                210                 215                 220

ctg gtg tgc acc ccc acc atc cac act gcc acc gtc aag gtc gtc ata     1083
Leu Val Cys Thr Pro Thr Ile His Thr Ala Thr Val Lys Val Val Ile
            225                 230                 235

cag gtc aac acc ttc atg tcc ttc ata ttc ccc atg gtg gtc atc tcg     1131
Gln Val Asn Thr Phe Met Ser Phe Ile Phe Pro Met Val Val Ile Ser
        240                 245                 250

gtc ctg aac acc atc atc gcc aac aag ctg acc gtc atg gta cgc cag     1179
Val Leu Asn Thr Ile Ile Ala Asn Lys Leu Thr Val Met Val Arg Gln
    255                 260                 265

gcg gcc gag cag ggc caa gtg tgc acg gtc ggg ggc gag cac agc aca     1227
Ala Ala Glu Gln Gly Gln Val Cys Thr Val Gly Gly Glu His Ser Thr
270                 275                 280                 285

ttc agc atg gcc atc gag cct ggc agg gtc cag gcc ctg cgg cac ggc     1275
Phe Ser Met Ala Ile Glu Pro Gly Arg Val Gln Ala Leu Arg His Gly
                290                 295                 300

gtg cgc gtc cta cgt gca gtg gtc atc gcc ttt gtg gtc tgc tgg ctg     1323
Val Arg Val Leu Arg Ala Val Val Ile Ala Phe Val Val Cys Trp Leu
            305                 310                 315

ccc tac cac gtg cgg cgc ctc atg ttc tgc tac atc tcg gat gag cag     1371
Pro Tyr His Val Arg Arg Leu Met Phe Cys Tyr Ile Ser Asp Glu Gln
        320                 325                 330

tgg act ccg ttc ctc tat gac ttc tac cac tac ttc tac atg gtg acc     1419
Trp Thr Pro Phe Leu Tyr Asp Phe Tyr His Tyr Phe Tyr Met Val Thr
    335                 340                 345
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aac gca ctc ttc tac gtc agc tcc acc atc aac ccc atc ctg tac aac     1467
Asn Ala Leu Phe Tyr Val Ser Ser Thr Ile Asn Pro Ile Leu Tyr Asn
350                 355                 360                 365

ctc gtc tct gcc aac ttc cgc cac atc ttc ctg gcc aca ctg gcc tgc     1515
Leu Val Ser Ala Asn Phe Arg His Ile Phe Leu Ala Thr Leu Ala Cys
                370                 375                 380

ctc tgc ccg gtg tgg cgg cgc agg agg aag agg cca gcc ttc tcg agg     1563
Leu Cys Pro Val Trp Arg Arg Arg Arg Lys Arg Pro Ala Phe Ser Arg
            385                 390                 395

aag gcc gac agc gtg tcc agc aac cac acc ctc tcc agc aat gcc acc     1611
Lys Ala Asp Ser Val Ser Ser Asn His Thr Leu Ser Ser Asn Ala Thr
        400                 405                 410

cgc gag acg ctg tac tag gctgtgcgcc ccggaacgtg tccaggagga            1659
Arg Glu Thr Leu Tyr
    415

gcctggccat gggtccttgc ccccgacaga cagagcagcc cccacccggg agccttgatg   1719

ggggtcaggc agaggccagc ctgcactgga gtctgaggcc tgggaccccc ccctcccacc   1779

ccctaaccca tgtttctcat tagtgtctcc cgggcctgtc cccaactcct ccccaccccc   1839

cccccatctc ctctttgaaa gccagaacaa gagagcgctc ctctcccaga taggaaaagg   1899

gcctctaaca aggagaaatt agtgtgcggc aaaaggcagt tttctttgtt ctcagactaa   1959

tggatggttc cagagaagga aatgaaatgt gctgggtggg gccgggcctc cggcggcccg   2019

gctgctgttc ccatgtccac atctctgagg cctgcacccc ctctgtctag ctcggggagt   2079

ccagccccag tcccgcaggc tccgtggctt tgggcctcac gtgcagaccc tgccatgcag   2139

acccatgccc ccctccccca ggcagctcca agaaagctcc ctgactcgcc ccttcaggcc   2199

tggcaagctg ggggcccatc gccgtgggga gtccctccca ccaccctcgc cgcaggcagc   2259

tgcagccccc agaggggacc acaagcccaa aaaggacaaa aatgggctgg cctggaatgg   2319

cccagacccc agcctccccc cctccctccc atcctcaccc aggccaaggc ccaggggctc   2379

tgccaggaca ccacatggga gggggctcag gcctcagcct caagatcttc agctgtggcc   2439

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tgagaaggag cggtgtgtcc aggcaccgct ggccggcagc cctgggctga ggcacagact   2739

catttgtcac cttctggcgg cggcagccct ggccccggcc tccaagcagt tgaaaaagct   2799

ggcgcctcct tggtctctag gatccaggct ccacagagca catgactagc caggcccctg   2859
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gcttaagaag gtcgcctaag cctaagagaa gacagtccca ggagaagctg gccgggacca 2919

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tgatgtggcc ccggaagctg gccctgcgtg ccatgagtgc gtcggtcatg gagtccggag 3999

cccctgagcc ggcccctggt gacggcacag ccctcacagc tcaaacgccc acccccactc 4059

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gcctcgatgt gg 4131

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<213> Homo sapiens

<400> 6

Met Arg Leu Asn Ser Ser Ala Pro Gly Thr Pro Gly Thr Pro Ala Ala
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Asp Pro Phe Gln Arg Ala Gln Ala Gly Leu Glu Glu Ala Leu Leu Ala
20 25 30

Pro Gly Phe Gly Asn Ala Ser Gly Asn Ala Ser Glu Arg Val Leu Ala

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        35                  40                  45

Ala Pro Ser Ser Glu Leu Asp Val Asn Thr Asp Ile Tyr Ser Lys Val
    50                  55                  60

Leu Val Thr Ala Val Tyr Leu Ala Leu Phe Val Val Gly Thr Val Gly
65                  70                  75                  80

Asn Thr Val Thr Ala Phe Thr Leu Ala Arg Lys Lys Ser Leu Gln Ser
                85                  90                  95

Leu Gln Ser Thr Val His Tyr His Leu Gly Ser Leu Ala Leu Ser Asp
            100                 105                 110

Leu Leu Thr Leu Leu Leu Ala Met Pro Val Glu Leu Tyr Asn Phe Ile
        115                 120                 125

Trp Val His His Pro Trp Ala Phe Gly Asp Ala Gly Cys Arg Gly Tyr
    130                 135                 140

Tyr Phe Leu Arg Asp Ala Cys Thr Tyr Ala Thr Ala Leu Asn Val Ala
145                 150                 155                 160

Ser Leu Ser Val Glu Arg Tyr Leu Ala Ile Cys His Pro Phe Lys Ala
                165                 170                 175

Lys Thr Leu Met Ser Arg Ser Arg Thr Lys Lys Phe Ile Ser Ala Ile
            180                 185                 190

Trp Leu Ala Ser Ala Leu Leu Thr Val Pro Met Leu Phe Thr Met Gly
        195                 200                 205

Glu Gln Asn Arg Ser Ala Asp Gly Gln His Ala Gly Gly Leu Val Cys
    210                 215                 220

Thr Pro Thr Ile His Thr Ala Thr Val Lys Val Val Ile Gln Val Asn
225                 230                 235                 240

Thr Phe Met Ser Phe Ile Phe Pro Met Val Val Ile Ser Val Leu Asn
                245                 250                 255

Thr Ile Ile Ala Asn Lys Leu Thr Val Met Val Arg Gln Ala Ala Glu
            260                 265                 270

Gln Gly Gln Val Cys Thr Val Gly Gly Glu His Ser Thr Phe Ser Met
        275                 280                 285
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```
Ala Ile Glu Pro Gly Arg Val Gln Ala Leu Arg His Gly Val Arg Val
    290                 295                 300

Leu Arg Ala Val Val Ile Ala Phe Val Val Cys Trp Leu Pro Tyr His
305                 310                 315                 320

Val Arg Arg Leu Met Phe Cys Tyr Ile Ser Asp Glu Gln Trp Thr Pro
                325                 330                 335

Phe Leu Tyr Asp Phe Tyr His Tyr Phe Tyr Met Val Thr Asn Ala Leu
            340                 345                 350

Phe Tyr Val Ser Ser Thr Ile Asn Pro Ile Leu Tyr Asn Leu Val Ser
        355                 360                 365

Ala Asn Phe Arg His Ile Phe Leu Ala Thr Leu Ala Cys Leu Cys Pro
    370                 375                 380

Val Trp Arg Arg Arg Arg Lys Arg Pro Ala Phe Ser Arg Lys Ala Asp
385                 390                 395                 400

Ser Val Ser Ser Asn His Thr Leu Ser Ser Asn Ala Thr Arg Glu Thr
                405                 410                 415

Leu Tyr
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<213> Artificial

<220>
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<210> 8
<211> 24
<212> DNA
<213> Artificial

<220>
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<400> 8
ggttttaaat gcagctccta tgtg 24

<210> 9
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<212> DNA
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<400> 9
ctgaacagtg ggtatcttcc tta 23

<210> 10
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gatggctctt gacttagagg ttc 23

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actgagaaca ttgacaacac agg 23

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aagagggaca gggacaagta gt 22

<210> 14
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atgccactgt tactgcttca g 21

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<400> 16
tgatacagag acatgaagtg agca 24

<210> 17
<211> 19
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<400> 17
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<210> 18
<211> 20
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<220>
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<400> 18
gaatcccaga agtctgaaca 20

<210> 19

<211> 19
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<400> 19
acggtcctct acagtctca 19

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<210> 25
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<220>
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<400> 25
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<210> 26
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<212> DNA
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<220>
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<400> 26
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<210> 27
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<220>
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<400> 27
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<210> 28
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<400> 28
caagtcagtg tacaggtaag c 21

<210> 29
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<220>
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<400> 29
gaagcagcac gacttcttc 19

<210> 30
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<220>
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<400> 30
cgtacgcgga atacttcga 19

<210> 31
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<212> DNA
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<220>
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<400> 31
gcgcgctttg taggattcg 19

<210> 32
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<220>
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<400> 32
gttagtgtac gaactggag 19

<210> 33
<211> 19
<212> DNA
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<220>
<223> A target sequence for siRNA

<400> 33
gtgtctctgt tggagatct 19

<210> 34
<211> 19
<212> DNA
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<220>
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<400> 34
gaaggcagtt gaccaacac 19

<210> 35
<211> 19
<212> DNA
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<220>
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<400> 35
cctctacctg tccagcatg 19

<210> 36
<211> 19
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<220>
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<400> 36
gttcatcagc gccatctgg 19

<210> 37
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<220>
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<400> 37
ggtcgtcata caggtcaac 19

<210> 38
<211> 32
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<220>
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<400> 38
ggaattccat gtggaacgcg acgcccagcg aa 32

<210> 39
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<212> DNA
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<220>
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<400> 39
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<210> 40
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<400> 40
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<210> 41
<211> 36
<212> DNA
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<220>
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<400> 41
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<210> 42
<211> 36
<212> DNA
<213> Artificial

<220>
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<400> 42
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<210> 43
<211> 39
<212> DNA
<213> Artificial

<220>
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<400> 43
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<210> 44
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<212> DNA
<213> Artificial

<220>

<223> An artificially synthesized primer sequence for PCR of H1RNA gene promoter region

<400> 44
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<210> 45
<211> 22
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<213> Artificial

<220>
<223> An artificially synthesized primer sequence for PCR of H1RNA gene promoter region

<400> 45
ccaaagggtt tctgcagttt ca 22

<210> 46
<211> 30

<212> DNA
<213> Artificial

<220>
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<400> 46
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<210> 47
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<212> DNA
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<400> 47
ctctatctcg agtgaggcgg aaagaacca 29

<210> 48
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<211> 34
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<213> Artificial

<220>
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<210> 52
<211> 51
<212> DNA
<213> Artificial

<220>
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<400> 52
aaaagttagt gtacgaactg gagtctcttg aactccagtt cgtacactaa c 51

<210> 53
<211> 47
<212> DNA
<213> Artificial

<220>
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gttagtgtac gaactggagt tcaagagact ccagttcgta cactaac 47

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<210> 63
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<210> 70
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<210> 79
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<400> 80
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<210> 81
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<220>
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<210> 82
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<400> 82
aagcgaaggt cagctaaata tcc 23

<210> 83
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<210> 84
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<400> 84
aagccctctt acttacaggg aaa 23

<210> 85
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<210> 88
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<220>
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<400> 92
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<210> 93

<211> 23
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<210> 94
<211> 23
<212> DNA
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<220>
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<400> 94
cacctcaatc tgaacaaggt tag 23

<210> 95
<211> 23
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<220>
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<400> 95
ggcctctcaa agtctggtag att 23

<210> 96
<211> 23
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<220>
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<210> 97
<211> 197
<212> PRT
<213> Artificial

<220>
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<400> 97

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Asp Leu Glu Ser Ile Phe Lys Asp Ala Lys Ile Pro Val Ser Gly Pro
20 25 30

Phe Leu Val Lys Thr Gly Tyr Ala Phe Val Asp Cys Pro Asp Glu Ser
35 40 45

Trp Ala Leu Lys Ala Ile Glu Ala Leu Ser Gly Lys Ile Glu Leu His
50 55 60

Gly Lys Pro Ile Glu Val Glu His Ser Val Pro Lys Arg Gln Arg Ile
65 70 75 80

Arg Lys Leu Gln Ile Arg Asn Ile Pro Pro His Leu Gln Trp Glu Val
85 90 95

Leu Asp Ser Leu Leu Val Gln Tyr Gly Val Val Glu Ser Cys Glu Gln
100 105 110

Val Asn Thr Asp Ser Glu Thr Ala Val Val Asn Val Thr Tyr Ser Ser
115 120 125

Lys Asp Gln Ala Arg Gln Ala Leu Asp Lys Leu Asn Gly Phe Gln Leu
130 135 140

Glu Asn Phe Thr Leu Lys Val Ala Tyr Ile Pro Asp Glu Met Ala Ala
145 150 155 160

Gln Gln Asn Pro Leu Gln Gln Pro Arg Gly Arg Arg Gly Leu Gly Gln
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180 185 190

Pro Cys Asp Leu Pro
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<210> 98
<211> 23
<212> DNA
<213> Artificial

<220>
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<400> 98
acgaactcat ttgctcactc ctt 23

<210> 99
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<220>
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<400> 99
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<210> 100
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<220>
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<400> 100
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<210> 101
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<400> 101
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<210> 102
<211> 22
<212> DNA
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<220>
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<400> 102
gggtggtctc ccataatagc aa 22

<210> 103
<211> 19
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<220>
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<400> 103
agcccacttt agagtatac 19

<210> 104
<211> 4168
<212> DNA
<213> Homo sapiens

<400> 104
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ttcttgtgct tggttcttac tgtgtttgtg tattttaaag gcgagaagac gaggggaaca 180

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Phe Leu Val Lys Thr Gly Tyr Ala Phe Val Asp Cys Pro Asp Glu Ser
35 40 45

Trp Ala Leu Lys Ala Ile Glu Ala Leu Ser Gly Lys Ile Glu Leu His
50 55 60

Gly Lys Pro Ile Glu Val Glu His Ser Val Pro Lys Arg Gln Arg Ile
65 70 75 80

Arg Lys Leu Gln Ile Arg Asn Ile Pro Pro His Leu Gln Trp Glu Val
85 90 95

Leu Asp Ser Leu Leu Val Gln Tyr Gly Val Val Glu Ser Cys Glu Gln
100 105 110

Val Asn Thr Asp Ser Glu Thr Ala Val Val Asn Val Thr Tyr Ser Ser
115 120 125

Lys Asp Gln Ala Arg Gln Ala Leu Asp Lys Leu Asn Gly Phe Gln Leu
130 135 140

Glu Asn Phe Thr Leu Lys Val Ala Tyr Ile Pro Asp Glu Met Ala Ala
145 150 155 160

Gln Gln Asn Pro Leu Gln Gln Pro Arg Gly Arg Arg Gly Leu Gly Gln
165 170 175

Arg Gly Ser Ser Arg Gln Gly Ser Pro Gly Ser Val Ser Lys Gln Lys
180 185 190

Pro Cys Asp Leu Pro Leu Arg Leu Leu Val Pro Thr Gln Phe Val Gly
195 200 205

Ala Ile Ile Gly Lys Glu Gly Ala Thr Ile Arg Asn Ile Thr Lys Gln
210 215 220

Thr Gln Ser Lys Ile Asp Val His Arg Lys Glu Asn Ala Gly Ala Ala
225 230 235 240

Glu Lys Ser Ile Thr Ile Leu Ser Thr Pro Glu Gly Thr Ser Ala Ala
245 250 255

Cys Lys Ser Ile Leu Glu Ile Met His Lys Glu Ala Gln Asp Ile Lys
260 265 270

Phe Thr Glu Glu Ile Pro Leu Lys Ile Leu Ala His Asn Asn Phe Val
275 280 285

Gly Arg Leu Ile Gly Lys Glu Gly Arg Asn Leu Lys Lys Ile Glu Gln
290 295 300

Asp Thr Asp Thr Lys Ile Thr Ile Ser Pro Leu Gln Glu Leu Thr Leu
305 310 315 320

Tyr Asn Pro Glu Arg Thr Ile Thr Val Lys Gly Asn Val Glu Thr Cys
325 330 335

Ala Lys Ala Glu Glu Glu Ile Met Lys Lys Ile Arg Glu Ser Tyr Glu
340 345 350

Asn Asp Ile Ala Ser Met Asn Leu Gln Ala His Leu Ile Pro Gly Leu

355 360 365

Asn Leu Asn Ala Leu Gly Leu Phe Pro Pro Thr Ser Gly Met Pro Pro
370 375 380

Pro Thr Ser Gly Pro Pro Ser Ala Met Thr Pro Pro Tyr Pro Gln Phe
385 390 395 400

Glu Gln Ser Glu Thr Glu Thr Val His Leu Phe Ile Pro Ala Leu Ser
405 410 415

Val Gly Ala Ile Ile Gly Lys Gln Gly Gln His Ile Lys Gln Leu Ser
420 425 430

Arg Phe Ala Gly Ala Ser Ile Lys Ile Ala Pro Ala Glu Ala Pro Asp
435 440 445

Ala Lys Val Arg Met Val Ile Ile Thr Gly Pro Pro Glu Ala Gln Phe
450 455 460

Lys Ala Gln Gly Arg Ile Tyr Gly Lys Ile Lys Glu Glu Asn Phe Val
465 470 475 480

Ser Pro Lys Glu Glu Val Lys Leu Glu Ala His Ile Arg Val Pro Ser
485 490 495

Phe Ala Ala Gly Arg Val Ile Gly Lys Gly Gly Lys Thr Val Asn Glu
500 505 510

Leu Gln Asn Leu Ser Ser Ala Glu Val Val Val Pro Arg Asp Gln Thr
515 520 525

Pro Asp Glu Asn Asp Gln Val Val Val Lys Ile Thr Gly His Phe Tyr
530 535 540

Ala Cys Gln Val Ala Gln Arg Lys Ile Gln Glu Ile Leu Thr Gln Val
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Arg Arg Lys

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gcccccgtcc ggggccctgg ctcggccccc aggttggagg agcccggagc ccgccttcgg 180

agctacggcc taacggcggc ggcgactgca gtctggaggg tccacacttg tgattctcaa 240

tggagagtga aaacgcagat tcata atg aaa act agc ccc cgt cgg cca ctg 292
Met Lys Thr Ser Pro Arg Arg Pro Leu
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att ctc aaa aga cgg agg ctg ccc ctt cct gtt caa aat gcc cca agt 340
Ile Leu Lys Arg Arg Arg Leu Pro Leu Pro Val Gln Asn Ala Pro Ser
10 15 20 25

gaa aca tca gag gag gaa cct aag aga tcc cct gcc caa cag gag tct 388
Glu Thr Ser Glu Glu Glu Pro Lys Arg Ser Pro Ala Gln Gln Glu Ser
30 35 40

aat caa gca gag gcc tcc aag gaa gtg gca gag tcc aac tct tgc aag 436
Asn Gln Ala Glu Ala Ser Lys Glu Val Ala Glu Ser Asn Ser Cys Lys
45 50 55

ttt cca gct ggg atc aag att att aac cac ccc acc atg ccc aac acg 484
Phe Pro Ala Gly Ile Lys Ile Ile Asn His Pro Thr Met Pro Asn Thr
60 65 70

caa gta gtg gcc atc ccc aac aat gct aat att cac agc atc atc aca 532
Gln Val Val Ala Ile Pro Asn Asn Ala Asn Ile His Ser Ile Ile Thr
75 80 85

gca ctg act gcc aag gga aaa gag agt ggc agt agt ggg ccc aac aaa 580
Ala Leu Thr Ala Lys Gly Lys Glu Ser Gly Ser Ser Gly Pro Asn Lys
90 95 100 105

ttc atc ctc atc agc tgt ggg gga gcc cca act cag cct cca gga ctc 628
Phe Ile Leu Ile Ser Cys Gly Gly Ala Pro Thr Gln Pro Pro Gly Leu
110 115 120

cgg cct caa acc caa acc agc tat gat gcc aaa agg aca gaa gtg acc 676
Arg Pro Gln Thr Gln Thr Ser Tyr Asp Ala Lys Arg Thr Glu Val Thr
125 130 135

ctg gag acc ttg gga cca aaa cct gca gct agg gat gtg aat ctt cct 724
Leu Glu Thr Leu Gly Pro Lys Pro Ala Ala Arg Asp Val Asn Leu Pro
140 145 150

aga cca cct gga gcc ctt tgc gag cag aaa cgg gag acc tgt gca gat 772
Arg Pro Pro Gly Ala Leu Cys Glu Gln Lys Arg Glu Thr Cys Ala Asp
155 160 165

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ggt gag gca gca ggc tgc act atc aac aat agc cta tcc aac atc cag      820
Gly Glu Ala Ala Gly Cys Thr Ile Asn Asn Ser Leu Ser Asn Ile Gln
170                 175                 180                 185

tgg ctt cga aag atg agt tct gat gga ctg ggc tcc cgc agc atc aag      868
Trp Leu Arg Lys Met Ser Ser Asp Gly Leu Gly Ser Arg Ser Ile Lys
                190                 195                 200

caa gag atg gag gaa aag gag aat tgt cac ctg gag cag cga cag gtt      916
Gln Glu Met Glu Glu Lys Glu Asn Cys His Leu Glu Gln Arg Gln Val
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aag gtt gag gag cct tcg aga cca tca gcg tcc tgg cag aac tct gtg      964
Lys Val Glu Glu Pro Ser Arg Pro Ser Ala Ser Trp Gln Asn Ser Val
        220                 225                 230

tct gag cgg cca ccc tac tct tac atg gcc atg ata caa ttc gcc atc     1012
Ser Glu Arg Pro Pro Tyr Ser Tyr Met Ala Met Ile Gln Phe Ala Ile
    235                 240                 245

aac agc act gag agg aag cgc atg act ttg aaa gac atc tat acg tgg     1060
Asn Ser Thr Glu Arg Lys Arg Met Thr Leu Lys Asp Ile Tyr Thr Trp
250                 255                 260                 265

att gag gac cac ttt ccc tac ttt aag cac att gcc aag cca ggc tgg     1108
Ile Glu Asp His Phe Pro Tyr Phe Lys His Ile Ala Lys Pro Gly Trp
                270                 275                 280

aag aac tcc atc cgc cac aac ctt tcc ctg cac gac atg ttt gtc cgg     1156
Lys Asn Ser Ile Arg His Asn Leu Ser Leu His Asp Met Phe Val Arg
            285                 290                 295

gag acg tct gcc aat ggc aag gtc tcc ttc tgg acc att cac ccc agt     1204
Glu Thr Ser Ala Asn Gly Lys Val Ser Phe Trp Thr Ile His Pro Ser
        300                 305                 310

gcc aac cgc tac ttg aca ttg gac cag gtg ttt aag cag cag aaa cga     1252
Ala Asn Arg Tyr Leu Thr Leu Asp Gln Val Phe Lys Gln Gln Lys Arg
    315                 320                 325

ccg aat cca gag ctc cgc cgg aac atg acc atc aaa acc gaa ctc ccc     1300
Pro Asn Pro Glu Leu Arg Arg Asn Met Thr Ile Lys Thr Glu Leu Pro
330                 335                 340                 345

ctg ggc gca cgg cgg aag atg aag cca ctg cta cca cgg gtc agc tca     1348
Leu Gly Ala Arg Arg Lys Met Lys Pro Leu Leu Pro Arg Val Ser Ser
                350                 355                 360

tac ctg gta cct atc cag ttc ccg gtg aac cag tca ctg gtg ttg cag     1396
Tyr Leu Val Pro Ile Gln Phe Pro Val Asn Gln Ser Leu Val Leu Gln
            365                 370                 375

ccc tcg gtg aag gtg cca ttg ccc ctg gcg gct tcc ctc atg agc tca     1444
Pro Ser Val Lys Val Pro Leu Pro Leu Ala Ala Ser Leu Met Ser Ser
        380                 385                 390

gag ctt gcc cgc cat agc aag cga gtc cgc att gcc ccc aag gtg ctg     1492
Glu Leu Ala Arg His Ser Lys Arg Val Arg Ile Ala Pro Lys Val Leu
    395                 400                 405
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cta gct gag gag ggg ata gct cct ctt tct tct gca gga cca ggg aaa     1540
Leu Ala Glu Glu Gly Ile Ala Pro Leu Ser Ser Ala Gly Pro Gly Lys
410                 415                 420                 425

gag gag aaa ctc ctg ttt gga gaa ggg ttt tct cct ttg ctt cca gtt     1588
Glu Glu Lys Leu Leu Phe Gly Glu Gly Phe Ser Pro Leu Leu Pro Val
                430                 435                 440

cag act atc aag gag gaa gaa atc cag cct ggg gag gaa atg cca cac     1636
Gln Thr Ile Lys Glu Glu Glu Ile Gln Pro Gly Glu Glu Met Pro His
            445                 450                 455

tta gcg aga ccc atc aaa gtg gag agc cct ccc ttg gaa gag tgg ccc     1684
Leu Ala Arg Pro Ile Lys Val Glu Ser Pro Pro Leu Glu Glu Trp Pro
        460                 465                 470

tcc ccg gcc cca tct ttc aaa gag gaa tca tct cac tcc tgg gag gat     1732
Ser Pro Ala Pro Ser Phe Lys Glu Glu Ser Ser His Ser Trp Glu Asp
    475                 480                 485

tcg tcc caa tct ccc acc cca aga ccc aag aag tcc tac agt ggg ctt     1780
Ser Ser Gln Ser Pro Thr Pro Arg Pro Lys Lys Ser Tyr Ser Gly Leu
490                 495                 500                 505

agg tcc cca acc cgg tgt gtc tcg gaa atg ctt gtg att caa cac agg     1828
Arg Ser Pro Thr Arg Cys Val Ser Glu Met Leu Val Ile Gln His Arg
                510                 515                 520

gag agg agg gag agg agc cgg tct cgg agg aaa cag cat cta ctg cct     1876
Glu Arg Arg Glu Arg Ser Arg Ser Arg Arg Lys Gln His Leu Leu Pro
            525                 530                 535

ccc tgt gtg gat gag ccg gag ctg ctc ttc tca gag ggg ccc agt act     1924
Pro Cys Val Asp Glu Pro Glu Leu Leu Phe Ser Glu Gly Pro Ser Thr
        540                 545                 550

tcc cgc tgg gcc gca gag ctc ccg ttc cca gca gac tcc tct gac cct     1972
Ser Arg Trp Ala Ala Glu Leu Pro Phe Pro Ala Asp Ser Ser Asp Pro
    555                 560                 565

gcc tcc cag ctc agc tac tcc cag gaa gtg gga gga cct ttt aag aca     2020
Ala Ser Gln Leu Ser Tyr Ser Gln Glu Val Gly Gly Pro Phe Lys Thr
570                 575                 580                 585

ccc att aag gaa acg ctg ccc atc tcc tcc acc ccg agc aaa tct gtc     2068
Pro Ile Lys Glu Thr Leu Pro Ile Ser Ser Thr Pro Ser Lys Ser Val
                590                 595                 600

ctc ccc aga acc cct gaa tcc tgg agg ctc acg ccc cca gcc aaa gta     2116
Leu Pro Arg Thr Pro Glu Ser Trp Arg Leu Thr Pro Pro Ala Lys Val
            605                 610                 615

ggg gga ctg gat ttc agc cca gta caa acc tcc cag ggt gcc tct gac     2164
Gly Gly Leu Asp Phe Ser Pro Val Gln Thr Ser Gln Gly Ala Ser Asp
        620                 625                 630

ccc ttg cct gac ccc ctg ggg ctg atg gat ctc agc acc act ccc ttg     2212
Pro Leu Pro Asp Pro Leu Gly Leu Met Asp Leu Ser Thr Thr Pro Leu
    635                 640                 645

caa agt gct ccc ccc ctt gaa tca ccg caa agg ctc ctc agt tca gaa     2260
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Gln Ser Ala Pro Pro Leu Glu Ser Pro Gln Arg Leu Leu Ser Ser Glu
650                 655                 660                 665

ccc tta gac ctc atc tcc gtc ccc ttt ggc aac tct tct ccc tca gat     2308
Pro Leu Asp Leu Ile Ser Val Pro Phe Gly Asn Ser Ser Pro Ser Asp
                670                 675                 680

ata gac gtc ccc aag cca ggc tcc ccg gag cca cag gtt tct ggc ctt     2356
Ile Asp Val Pro Lys Pro Gly Ser Pro Glu Pro Gln Val Ser Gly Leu
            685                 690                 695

gca gcc aat cgt tct ctg aca gaa ggc ctg gtc ctg gac aca atg aat     2404
Ala Ala Asn Arg Ser Leu Thr Glu Gly Leu Val Leu Asp Thr Met Asn
        700                 705                 710

gac agc ctc agc aag atc ctg ctg gac atc agc ttt cct ggc ctg gac     2452
Asp Ser Leu Ser Lys Ile Leu Leu Asp Ile Ser Phe Pro Gly Leu Asp
    715                 720                 725

gag gac cca ctg ggc cct gac aac atc aac tgg tcc cag ttt att cct     2500
Glu Asp Pro Leu Gly Pro Asp Asn Ile Asn Trp Ser Gln Phe Ile Pro
730                 735                 740                 745

gag cta cag tag agccctgccc ttgcccctgt gctcaagctg tccaccatcc         2552
Glu Leu Gln

cgggcactcc aaggctcagt gcaccccaag cctctgagtg aggacagcag gcagggactg   2612

ttctgctcct catagctccc tgctgcctga ttatgcaaaa gtagcagtca caccctagcc   2672

actgctggga ccttgtgttc cccaagagta tctgattcct ctgctgtccc tgccaggagc   2732

tgaagggtgg gaacaacaaa ggcaatggtg aaaagagatt aggaaccccc cagcctgttt   2792

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gaaagggccc ctgacctgcc tggcttcctt agcttgcccc tcagctttgc aaagagccac   3392

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Lys Arg Ser Pro Ala Gln Gln Glu Ser Asn Gln Ala Glu Ala Ser Lys
35 40 45

Glu Val Ala Glu Ser Asn Ser Cys Lys Phe Pro Ala Gly Ile Lys Ile
50 55 60

Ile Asn His Pro Thr Met Pro Asn Thr Gln Val Val Ala Ile Pro Asn
65 70 75 80

Asn Ala Asn Ile His Ser Ile Ile Thr Ala Leu Thr Ala Lys Gly Lys
85 90 95

Glu Ser Gly Ser Ser Gly Pro Asn Lys Phe Ile Leu Ile Ser Cys Gly
100 105 110

Gly Ala Pro Thr Gln Pro Pro Gly Leu Arg Pro Gln Thr Gln Thr Ser
115 120 125

Tyr Asp Ala Lys Arg Thr Glu Val Thr Leu Glu Thr Leu Gly Pro Lys
130 135 140

Pro Ala Ala Arg Asp Val Asn Leu Pro Arg Pro Pro Gly Ala Leu Cys
145 150 155 160

Glu Gln Lys Arg Glu Thr Cys Ala Asp Gly Glu Ala Ala Gly Cys Thr
165 170 175

Ile Asn Asn Ser Leu Ser Asn Ile Gln Trp Leu Arg Lys Met Ser Ser
180 185 190

Asp Gly Leu Gly Ser Arg Ser Ile Lys Gln Glu Met Glu Glu Lys Glu
195 200 205

Asn Cys His Leu Glu Gln Arg Gln Val Lys Val Glu Glu Pro Ser Arg
210 215 220

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Pro Ser Ala Ser Trp Gln Asn Ser Val Ser Glu Arg Pro Pro Tyr Ser
225                 230                 235                 240

Tyr Met Ala Met Ile Gln Phe Ala Ile Asn Ser Thr Glu Arg Lys Arg
                245                 250                 255

Met Thr Leu Lys Asp Ile Tyr Thr Trp Ile Glu Asp His Phe Pro Tyr
            260                 265                 270

Phe Lys His Ile Ala Lys Pro Gly Trp Lys Asn Ser Ile Arg His Asn
        275                 280                 285

Leu Ser Leu His Asp Met Phe Val Arg Glu Thr Ser Ala Asn Gly Lys
    290                 295                 300

Val Ser Phe Trp Thr Ile His Pro Ser Ala Asn Arg Tyr Leu Thr Leu
305                 310                 315                 320

Asp Gln Val Phe Lys Gln Gln Lys Arg Pro Asn Pro Glu Leu Arg Arg
                325                 330                 335

Asn Met Thr Ile Lys Thr Glu Leu Pro Leu Gly Ala Arg Arg Lys Met
            340                 345                 350

Lys Pro Leu Leu Pro Arg Val Ser Ser Tyr Leu Val Pro Ile Gln Phe
        355                 360                 365

Pro Val Asn Gln Ser Leu Val Leu Gln Pro Ser Val Lys Val Pro Leu
    370                 375                 380

Pro Leu Ala Ala Ser Leu Met Ser Ser Glu Leu Ala Arg His Ser Lys
385                 390                 395                 400

Arg Val Arg Ile Ala Pro Lys Val Leu Leu Ala Glu Glu Gly Ile Ala
                405                 410                 415

Pro Leu Ser Ser Ala Gly Pro Gly Lys Glu Glu Lys Leu Leu Phe Gly
            420                 425                 430

Glu Gly Phe Ser Pro Leu Leu Pro Val Gln Thr Ile Lys Glu Glu Glu
        435                 440                 445

Ile Gln Pro Gly Glu Glu Met Pro His Leu Ala Arg Pro Ile Lys Val
    450                 455                 460
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Glu Ser Pro Pro Leu Glu Glu Trp Pro Ser Pro Ala Pro Ser Phe Lys
465 470 475 480

Glu Glu Ser Ser His Ser Trp Glu Asp Ser Ser Gln Ser Pro Thr Pro
485 490 495

Arg Pro Lys Lys Ser Tyr Ser Gly Leu Arg Ser Pro Thr Arg Cys Val
500 505 510

Ser Glu Met Leu Val Ile Gln His Arg Glu Arg Arg Glu Arg Ser Arg
515 520 525

Ser Arg Arg Lys Gln His Leu Leu Pro Pro Cys Val Asp Glu Pro Glu
530 535 540

Leu Leu Phe Ser Glu Gly Pro Ser Thr Ser Arg Trp Ala Ala Glu Leu
545 550 555 560

Pro Phe Pro Ala Asp Ser Ser Asp Pro Ala Ser Gln Leu Ser Tyr Ser
565 570 575

Gln Glu Val Gly Gly Pro Phe Lys Thr Pro Ile Lys Glu Thr Leu Pro
580 585 590

Ile Ser Ser Thr Pro Ser Lys Ser Val Leu Pro Arg Thr Pro Glu Ser
595 600 605

Trp Arg Leu Thr Pro Pro Ala Lys Val Gly Gly Leu Asp Phe Ser Pro
610 615 620

Val Gln Thr Ser Gln Gly Ala Ser Asp Pro Leu Pro Asp Pro Leu Gly
625 630 635 640

Leu Met Asp Leu Ser Thr Thr Pro Leu Gln Ser Ala Pro Pro Leu Glu
645 650 655

Ser Pro Gln Arg Leu Leu Ser Ser Glu Pro Leu Asp Leu Ile Ser Val
660 665 670

Pro Phe Gly Asn Ser Ser Pro Ser Asp Ile Asp Val Pro Lys Pro Gly
675 680 685

Ser Pro Glu Pro Gln Val Ser Gly Leu Ala Ala Asn Arg Ser Leu Thr
690 695 700

Glu Gly Leu Val Leu Asp Thr Met Asn Asp Ser Leu Ser Lys Ile Leu
705 710 715 720

Leu Asp Ile Ser Phe Pro Gly Leu Asp Glu Asp Pro Leu Gly Pro Asp
725 730 735

Asn Ile Asn Trp Ser Gln Phe Ile Pro Glu Leu Gln
740 745

<210> 108
<211> 19
<212> DNA
<213> Artificial

<220>
<223> A target sequence for siRNA.

<400> 108
gcagcagaaa cgaccgaat 19

<210> 109
<211> 51
<212> DNA
<213> Artificial

<220>
<223> An artificially synthesized oligonucleotide sequence for siRNA.

<400> 109
tcccgcagca gaaacgaccg aatttcaaga gaattcggtc gtttctgctg c 51

<210> 110
<211> 51
<212> DNA
<213> Artificial

<220>
<223> An artificially synthesized oligonucleotide sequence for siRNA.

<400> 110
aaaagcagca gaaacgaccg aattctcttg aaattcggtc gtttctgctg c 51

<210> 111
<211> 47
<212> DNA
<213> Artificial

<220>
<223> An artificially synthesized hairpin siRNA sequence.

<400> 111
gcagcagaaa cgaccgaatt tcaagagaat tcggtcgttt ctgctgc 47

<210> 112
<211> 2931
<212> DNA
<213> Homo sapiens

<220>
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<400> 112
aggggagcg gagggaggtg tttctgtcag ttccggctgt ttgttcggga agtggatccg 60

ccgctgccgg agcagcccga agggagctgc ggatcgcgag gccagtaccg accccgcccg 120

cccgcgcgca ccgcccccgc ccgcc atg gcc cgg gac tac gac cac ctc ttc 172
Met Ala Arg Asp Tyr Asp His Leu Phe
1 5

aag ctg ctc atc atc ggc gac agc ggt gtg ggc aag agc agt tta ctg 220
Lys Leu Leu Ile Ile Gly Asp Ser Gly Val Gly Lys Ser Ser Leu Leu
10 15 20 25

ttg cgt ttt gca gac aac act ttc tca ggc agc tac atc acc acg atc 268
Leu Arg Phe Ala Asp Asn Thr Phe Ser Gly Ser Tyr Ile Thr Thr Ile
30 35 40

gga gtg gat ttc aag atc cgg acc gtg gag atc aac ggg gag aag gtg 316
Gly Val Asp Phe Lys Ile Arg Thr Val Glu Ile Asn Gly Glu Lys Val
45 50 55

aag ctg cag atc tgg gac aca gcg ggg cag gag cgc ttc cgc acc atc 364
Lys Leu Gln Ile Trp Asp Thr Ala Gly Gln Glu Arg Phe Arg Thr Ile
60 65 70

acc tcc acg tat tat cgg ggg acc cac ggg gtc att gtg gtt tac gac 412
Thr Ser Thr Tyr Tyr Arg Gly Thr His Gly Val Ile Val Val Tyr Asp
75 80 85

gtc acc agt gcc gag tcc ttt gtc aac gtc aag cgg tgg ctt cac gaa 460
Val Thr Ser Ala Glu Ser Phe Val Asn Val Lys Arg Trp Leu His Glu
90 95 100 105

atc aac cag aac tgt gat gat gtg tgc cga ata tta gtg ggt aat aag 508
Ile Asn Gln Asn Cys Asp Asp Val Cys Arg Ile Leu Val Gly Asn Lys
110 115 120

aat gac gac cct gag cgg aag gtg gtg gag acg gaa gat gcc tac aaa 556
Asn Asp Asp Pro Glu Arg Lys Val Val Glu Thr Glu Asp Ala Tyr Lys
125 130 135

ttc gcc ggg cag atg ggc atc cag ttg ttc gag acc agc gcc aag gag 604
Phe Ala Gly Gln Met Gly Ile Gln Leu Phe Glu Thr Ser Ala Lys Glu
140 145 150

aat gtc aac gtg gaa gag atg ttc aac tgc atc acg gag ctg gtc ctc 652
Asn Val Asn Val Glu Glu Met Phe Asn Cys Ile Thr Glu Leu Val Leu
155 160 165

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cga gca aag aaa gac aac ctg gca aaa cag cag cag caa caa cag aac      700
Arg Ala Lys Lys Asp Asn Leu Ala Lys Gln Gln Gln Gln Gln Asn
170                 175                 180                 185

gat gtg gtg aag ctc acg aag aac agt aaa cga aag aaa cgc tgc tgc      748
Asp Val Val Lys Leu Thr Lys Asn Ser Lys Arg Lys Lys Arg Cys Cys
                190                 195                 200

taa tggcacccag tccactgcag agactgcact gcggtccctc ccccagcccg           801

aggcccacgg aggttcctcg ggggacagtc tcagtttcgt gccgttattt aaagaattct    861

ctccatgttt ttgtatcggg aggtgccatc ggcacttcct cccccgccct cctcgagtgc    921

caagaaggtg ttggaccagc ccgcccttcc ctactggtgc cccctcctcc ccggccaagg    981

cgcctggacc tggcgaggac gctgcccgcc gagcggactg attcgcagag tctgtacata   1041

gtgtatattg ctctacccgg ccgcacacca cgtcctgctc tggcttttgc cttcttgatg   1101

ccagcctgct gcaacagacc ctccccgcgc ccctccccag cccatcttac tgcaagcagc   1161

gtcctgagga gacagcggca cgttctagct gcgtctgcgg ccagcccgtg ccagtggagt   1221

gggctccgcg ttgctcattc tctccgacag gttgtcagcc tctgtccccg ctgcacaggg   1281

tcttgccccc tctccggggc ctgtgccagc tcccttccct ccccgttgtc ctgtccccac   1341

agccattctg ggagctgggg aacctggtct caaggcaggc cctgcagttc cacagaggtg   1401

gcaggtcttg ccctttggcc aacagatttc ttgtcctgcc ttctagatgc ctctgagctc   1461

caaacccagg gcagccatgg cttctcattt acaccaacag gtttcagttc caacagaaag   1521

gtcggggtag gttcgtgcag agatggggct ggcaggggag ctatgggagg attattttaa   1581

cagatcaaga aaatgaagcc aaatcaagtg aattaaattc ctcacaatta ttttctttcc   1641

ctgaggtttg attggcacag cagcaaaagt tgaggccacc ccacttgtgt ccactgtttt   1701

tagaaaaaaa tgaatggctt cctgccattg tggggctgga ctcttgggct ttcttggtgg   1761

gagcggagaa ggggcctccc acccttgtcc gagttgcctc ccactggagg tcaggagtct   1821

acactgcagc ctcgggcact gtggggagtg catgcctggg gcctctgggt ggggaccatg   1881

gacaggccct ggtcactgtc ctaacctttg tcaggacaaa ggtagcaaga ggatttcctg   1941

gcgggtggga aggaatggct ggggcggcca gttttgacac gccccagtgc cctggagaac   2001

aaccagggtc atctgcactt gatgactgct ccccgacccc cagcccggac acctcattcc   2061

cctcccacta cagggatcaa gtgacctggg aagaaccgag tttaacacca ggatgtgttt   2121

ccttagattt cctttcctag gcgatttcca gggagagccc tgattggaca atcacatcac   2181

agatcacact gcagtttcca tgttagcact gtggatgggt ttttaatcaa taaaaactgg   2241

gggtttcttc tcaccgactc tccacttgcc caaactgcca aaagctggtg attctgggac   2301

aggccttcac tttggagcca cgggatgggg tgggggagcc ccatgggcct gggaaggagg   2361
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gtgctgtgga gggggctgca gggctgacca gcaggcagcc tcatctggtc gggggcgggg 2421

gcggcaggag cagaagcggg gtctccgtcc ttgggactgt cctggttggc cacgggccct 2481

gaggatgcac ggtgcctggg gctcctgtgc cggtgggcgg ggggcatgct ggcctctgag 2541

cgatcaggcg aggccagcga gggtgtgctt gcaaattcaa gcaataagag gggggttcct 2601

gggggcttcc agcccaggct agaagccccc atggcttctg gcagctggac atcagcccca 2661

ggtattgggg tgattttggt catgacagtg tgcctgtccc actgttacac gcatgaatgg 2721

gggttatggg gtgggggtgg ggactcaggg ctggaccgac gtcctagtgg acctgatgtg 2781

aaattcctgt caaacaaaca ccacttttca atggtttgct aggagtattt ctgtattgaa 2841

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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2931

<210> 113
<211> 201
<212> PRT
<213> Homo sapiens

<400> 113

Met Ala Arg Asp Tyr Asp His Leu Phe Lys Leu Leu Ile Ile Gly Asp
1 5 10 15

Ser Gly Val Gly Lys Ser Ser Leu Leu Leu Arg Phe Ala Asp Asn Thr
20 25 30

Phe Ser Gly Ser Tyr Ile Thr Thr Ile Gly Val Asp Phe Lys Ile Arg
35 40 45

Thr Val Glu Ile Asn Gly Glu Lys Val Lys Leu Gln Ile Trp Asp Thr
50 55 60

Ala Gly Gln Glu Arg Phe Arg Thr Ile Thr Ser Thr Tyr Tyr Arg Gly
65 70 75 80

Thr His Gly Val Ile Val Val Tyr Asp Val Thr Ser Ala Glu Ser Phe
85 90 95

Val Asn Val Lys Arg Trp Leu His Glu Ile Asn Gln Asn Cys Asp Asp
100 105 110

Val Cys Arg Ile Leu Val Gly Asn Lys Asn Asp Asp Pro Glu Arg Lys
115 120 125

Val Val Glu Thr Glu Asp Ala Tyr Lys Phe Ala Gly Gln Met Gly Ile
130 135 140

Gln Leu Phe Glu Thr Ser Ala Lys Glu Asn Val Asn Val Glu Glu Met
145 150 155 160

Phe Asn Cys Ile Thr Glu Leu Val Leu Arg Ala Lys Lys Asp Asn Leu
165 170 175

Ala Lys Gln Gln Gln Gln Gln Asn Asp Val Val Lys Leu Thr Lys
180 185 190

Asn Ser Lys Arg Lys Lys Arg Cys Cys
195 200

<210> 114
<211> 19
<212> DNA
<213> Artificial

<220>
<223> A target sequence for siRNA.

<400> 114
gagatgttca actgcatca 19

<210> 115
<211> 51
<212> DNA
<213> Artificial

<220>
<223> An artificially synthesized oligonucleotide sequence for siRNA.

<400> 115
tcccgagatg ttcaactgca tcattcaaga gatgatgcag ttgaacatct c 51

<210> 116
<211> 51
<212> DNA
<213> Artificial

<220>
<223> An artificially synthesized oligonucleotide sequence for siRNA.

<400> 116
aaaagagatg ttcaactgca tcatctcttg aatgatgcag ttgaacatct c 51

<210> 117
<211> 47
<212> DNA
<213> Artificial

<220>
<223> An artificially synthesized hairpin siRNA sequence.

<400> 117
gagatgttca actgcatcat tcaagagatg atgcagttga acatctc 47

<210> 118
<211> 22
<212> DNA
<213> Artificial

<220>
<223> An artificially synthesized primer sequence for RT-PCR.

<400> 118
aaaaagggga tgcctagaac tc 22

<210> 119
<211> 21
<212> DNA
<213> Artificial

<220>
<223> An artificially synthesized primer sequence for RT-PCR.

<400> 119
ctttcagcac gtcaaggaca t 21

<210> 120
<211> 23
<212> DNA
<213> Artificial

<220>
<223> An artificially synthesized primer sequence for RT-PCR.

<400> 120
acacctacga aggtacacat gac 23

<210> 121

<211> 23
<212> DNA
<213> Artificial

<220>
<223> An artificially synthesized primer sequence for RT-PCR.

<400> 121
gctatttcag ggtaaatgga gtc 23

<210> 122
<211> 23
<212> DNA
<213> Artificial

<220>
<223> An artificially synthesized primer sequence for RT-PCR.

<400> 122
cagagatgga ggatgtcaat aac 23

<210> 123
<211> 23
<212> DNA
<213> Artificial

<220>
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<400> 123
catagcagct ttaaagagac acg 23

<210> 124
<211> 21
<212> DNA
<213> Artificial

<220>
<223> An artificially synthesized primer sequence for RT-PCR.

<400> 124
ccaccataac agtggagtgg g 21

<210> 125
<211> 24
<212> DNA
<213> Artificial

<220>
<223> An artificially synthesized primer sequence for RT-PCR.

<400> 125
cagttacagg tgtatgactg ggag 24

<210> 126
<211> 23
<212> DNA
<213> Artificial

<220>
<223> An artificially synthesized primer sequence for RT-PCR.

<400> 126
ctgaatacaa cttcctgttt gcc 23

<210> 127
<211> 23
<212> DNA
<213> Artificial

<220>

<223> An artificially synthesized primer sequence for RT-PCR.

<400> 127
gaccacagaa ttaccaaaac tgc 23